RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/559,867

DATE: 07/20/2001
TIME: 14:19:36 2001

Input Set : A:\600221nc.app
Output Set: N:\CRF3\07202001\I559867.raw

```
   3 <110> APPLICANT: Young, Michael W
   4        Kloss, Brian
   5        Blau, Justin
   6        Price, Jeffrey
   7        Takahashi, Joseph S.
   8        Philip, Lowrey L.
  10 <120> TITLE OF INVENTION: A NOVEL CLOCK GENE AND METHODS OF USE THEREOF
  12 <130> FILE REFERENCE: 600-1-221NCP
C-> 14 <140> CURRENT APPLICATION NUMBER: US/09/559,867
C-> 15 <141> CURRENT FILING DATE: 2000-04-26
  17 <150> PRIOR APPLICATION NUMBER: 60/090,068
  18 <151> PRIOR FILING DATE: 1998-06-19
  20 <150> PRIOR APPLICATION NUMBER: 09/335,983
  21 <151> PRIOR FILING DATE: 1999-06-18
  23 <160> NUMBER OF SEQ ID NOS: 42
  25 <170> SOFTWARE: PatentIn Ver. 2.0
  27 <210> SEQ ID NO: 1
  28 <211> LENGTH: 1520
  29 <212> TYPE: DNA
  30 <213> ORGANISM: Drosophila melanogaster
  32 <400> SEQUENCE: 1
  33 aaatccgagg aaccgaggag tccgaactct accacacaga aacccacaga aacagacgta 60
  34 acaaaatgga gctgcgcgtg ggtaacaaat atcgcctggg ccgcaagata ggatcgggat 120
  35 cgttcggcga catctacctg ggcaccacga tcaacactgg cgaggaggtg gccatcaagc 180
  36 tggagtgcat ccgcaccaaa cacccccagc tgcacatcga gtcaaagttc tacaagacga 240
  37 tgcagggtgg cataggcata ccccgcataa tctggtgcgg cagcgagggc gactacaatg 300
  38 tgatggtgat ggagctactc ggaccctcgc tggaggacct cttcaacttt tgttcacgcc 360
  39 gcttttcgtt gaagacggtt ctgctgctgg cggaccagat gatctcccgc atcgattaca 420
  40 tacactcgcg ggacttcatc catcgcgaca tcaagccgga taacttcctc atgggtcttg 480
  41 gcaagaaggg caacctggtg tacatcattg actttggcct ggccaagaaa ttccgcgatg 540
  42 cccggtcgct gaagcacatt ccctatcggg aaaacaagaa cctcacgggc actgcccgct 600
  43 atgcctccat caacacacat ttgggcattg agcaatcgcg tcgtgacgac ctggagtccc 660
  44 tgggttacgt cctaatgtac ttcaatctgg gcgccttgcc ctggcagggc ttaaaggcag 720
  45 ccaacaagag gcaaaagtac gagaggatct cggagaagaa gctgtccacc tcgattgtgg 780
  46 tgctgtgcaa gggcttcccc agcgagttcg tcaactatct gaacttctgt cgccagatgc 840
  47 atttcgacca gcgtcccgat tactgccacc tgcgcaaact cttccgcaac ttgttccacc 900
  48 gtttgggctt cacttacgac tatgtgtttg actggaacct gcttaagttt ggcggacctc 960
  49 gcaatcccca ggcgattcag caggcgcagg acggagcgga cggccaggcg ggtcatgatg 1020
  50 cggtggccgc agcagcggcg gtggcagcag cggcagccgc ctcctcgcat caacagcagc 1080
  51 agcacaaggt caatgcggcg ctgggtggcg gaggaggcag tcgtgcgcaa cagcaactcc 1140
  52 agggcggcca aacgctggcg atgctgggcg gcaatggagg cggtaacggc agccaactga 1200
  53 tcggcggcaa cggactcaac atggacgatt cgatggcggc caccaactcg tcgagaccgc 1260
  54 cgtacgacac gccggagcgt cggccctcga tacggatgcg gcagggaggc ggtggtggcg 1320
  55 gcggtggagt gggcgtaggc ggtatgcaga gcggcggagg gggcggtggc gtggggaacg 1380
  56 ccaaataata ttttatcgtt taggttgcga cgctggacac gacacagtag acaaacaaca 1440
  57 acagaactca acaaactata catgtagtat atatagttat atatacctaa tatatataat 1500
  58 acttgcttta tatatgcggt 1520
```

ENTERED
See page 5

RAW SEQUENCE LISTING   DATE: 07/20/2001
PATENT APPLICATION: US/09/559,867   TIME: 14:19:36

Input Set : A:\600221nc.app
Output Set: N:\CRF3\07202001\I559867.raw

```
60 <210> SEQ ID NO: 2
61 <211> LENGTH: 440
62 <212> TYPE: PRT
63 <213> ORGANISM: Drosophila melanogaster
65 <400> SEQUENCE: 2
66 Met Glu Leu Arg Val Gly Asn Lys Tyr Arg Leu Gly Arg Lys Ile Gly
67  1               5                  10                  15
69 Ser Gly Ser Phe Gly Asp Ile Tyr Leu Gly Thr Thr Ile Asn Thr Gly
70              20                  25                  30
72 Glu Glu Val Ala Ile Lys Leu Glu Cys Ile Arg Thr Lys His Pro Gln
73          35                  40                  45
75 Leu His Ile Glu Ser Lys Phe Tyr Lys Thr Met Gln Gly Gly Ile Gly
76      50                  55                  60
78 Ile Pro Arg Ile Ile Trp Cys Gly Ser Glu Gly Asp Tyr Asn Val Met
79  65              70                  75                  80
81 Val Met Glu Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Asn Phe Cys
82              85                  90                  95
84 Ser Arg Arg Phe Ser Leu Lys Thr Val Leu Leu Leu Ala Asp Gln Met
85              100                 105                 110
87 Ile Ser Arg Ile Asp Tyr Ile His Ser Arg Asp Phe Ile His Arg Asp
88          115                 120                 125
90 Ile Lys Pro Asp Asn Phe Leu Met Gly Leu Gly Lys Lys Gly Asn Leu
91      130                 135                 140
93 Val Tyr Ile Ile Asp Phe Gly Leu Ala Lys Lys Phe Arg Asp Ala Arg
94 145                 150                 155                 160
96 Ser Leu Lys His Ile Pro Tyr Arg Glu Asn Lys Asn Leu Thr Gly Thr
97              165                 170                 175
99 Ala Arg Tyr Ala Ser Ile Asn Thr His Leu Gly Ile Glu Gln Ser Arg
100             180                 185                 190
102 Arg Asp Asp Leu Glu Ser Leu Gly Tyr Val Leu Met Tyr Phe Asn Leu
103             195                 200                 205
105 Gly Ala Leu Pro Trp Gln Gly Leu Lys Ala Ala Asn Lys Arg Gln Lys
106     210                 215                 220
108 Tyr Glu Arg Ile Ser Glu Lys Lys Leu Ser Thr Ser Ile Val Val Leu
109 225                 230                 235                 240
111 Cys Lys Gly Phe Pro Ser Glu Phe Val Asn Tyr Leu Asn Phe Cys Arg
112             245                 250                 255
114 Gln Met His Phe Asp Gln Arg Pro Asp Tyr Cys His Leu Arg Lys Leu
115             260                 265                 270
117 Phe Arg Asn Leu Phe His Arg Leu Gly Phe Thr Tyr Asp Tyr Val Phe
118     275                 280                 285
120 Asp Trp Asn Leu Leu Lys Phe Gly Gly Pro Arg Asn Pro Gln Ala Ile
121     290                 295                 300
123 Gln Gln Ala Gln Asp Gly Ala Asp Gly Gln Ala Gly His Asp Ala Val
124 305                 310                 315                 320
126 Ala Ala Ala Ala Ala Val Ala Ala Ala Ala Ala Ala Ser Ser His Gln
127             325                 330                 335
129 Gln Gln Gln His Lys Val Asn Ala Ala Leu Gly Gly Gly Gly Gly Ser
130             340                 345                 350
```

```
132 Arg Ala Gln Gln Gln Leu Gln Gly Gly Gln Thr Leu Ala Met Leu Gly
133         355             360             365
135 Gly Asn Gly Gly Gly Asn Gly Ser Gln Leu Ile Gly Gly Asn Gly Leu
136     370             375             380
138 Asn Met Asp Asp Ser Met Ala Ala Thr Asn Ser Ser Arg Pro Pro Tyr
139 385             390             395             400
141 Asp Thr Pro Glu Arg Arg Pro Ser Ile Arg Met Arg Gln Gly Gly Gly
142             405             410             415
144 Gly Gly Gly Gly Gly Val Gly Val Gly Gly Met Gln Ser Gly Gly Gly
145         420             425             430
147 Gly Gly Gly Val Gly Asn Ala Lys
148     435             440
152 <210> SEQ ID NO: 3
153 <211> LENGTH: 440
154 <212> TYPE: PRT
155 <213> ORGANISM: Drosophila melanogaster
157 <400> SEQUENCE: 3
158 Met Glu Leu Arg Val Gly Asn Lys Tyr Arg Leu Gly Arg Lys Ile Gly
159  1             5               10              15
161 Ser Gly Ser Phe Gly Asp Ile Tyr Leu Gly Thr Thr Ile Asn Thr Gly
162         20              25              30
164 Glu Glu Val Ala Ile Lys Leu Glu Cys Ile Arg Thr Lys His Ser Gln
165         35              40              45
167 Leu His Ile Glu Ser Lys Phe Tyr Lys Thr Met Gln Gly Gly Ile Gly
168     50              55              60
170 Ile Pro Arg Ile Ile Trp Cys Gly Ser Glu Gly Asp Tyr Asn Val Met
171 65              70              75              80
173 Val Met Glu Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Asn Phe Cys
174             85              90              95
176 Ser Arg Arg Phe Ser Leu Lys Thr Val Leu Leu Leu Ala Asp Gln Met
177         100             105             110
179 Ile Ser Arg Ile Asp Tyr Ile His Ser Arg Asp Phe Ile His Arg Asp
180         115             120             125
182 Ile Lys Pro Asp Asn Phe Leu Met Gly Leu Gly Lys Lys Gly Asn Leu
183     130             135             140
185 Val Tyr Ile Ile Asp Phe Gly Leu Ala Lys Lys Phe Arg Asp Ala Arg
186 145             150             155             160
188 Ser Leu Lys His Ile Pro Tyr Arg Glu Asn Lys Asn Leu Thr Gly Thr
189         165             170             175
191 Ala Arg Tyr Ala Ser Ile Asn Thr His Leu Gly Ile Glu Gln Ser Arg
192         180             185             190
194 Arg Asp Asp Leu Glu Ser Leu Gly Tyr Val Leu Met Tyr Phe Asn Leu
195         195             200             205
197 Gly Ala Leu Pro Trp Gln Gly Leu Lys Ala Ala Asn Lys Arg Gln Lys
198     210             215             220
200 Tyr Glu Arg Ile Ser Glu Lys Lys Leu Ser Thr Ser Ile Val Val Leu
201 225             230             235             240
203 Cys Lys Gly Phe Pro Ser Glu Phe Val Asn Tyr Leu Asn Phe Cys Arg
204             245             250             255
```

```
206 Gln Met His Phe Asp Gln Arg Pro Asp Tyr Cys His Leu Arg Lys Leu
207         260             265             270
209 Phe Arg Asn Leu Phe His Arg Leu Gly Phe Thr Tyr Asp Tyr Val Phe
210         275             280             285
212 Asp Trp Asn Leu Leu Lys Phe Gly Gly Pro Arg Asn Pro Gln Ala Ile
213     290             295             300
215 Gln Gln Ala Gln Asp Gly Ala Asp Gly Gln Ala Gly His Asp Ala Val
216 305             310             315             320
218 Ala Ala Ala Ala Ala Val Ala Ala Ala Ala Ala Ala Ser Ser His Gln
219             325             330             335
221 Gln Gln Gln His Lys Val Asn Ala Ala Leu Gly Gly Gly Gly Gly Ser
222         340             345             350
224 Arg Ala Gln Gln Gln Leu Gln Gly Gly Gln Thr Leu Ala Met Leu Gly
225         355             360             365
227 Gly Asn Gly Gly Gly Asn Gly Ser Gln Leu Ile Gly Gly Asn Gly Leu
228     370             375             380
230 Asn Met Asp Asp Ser Met Ala Ala Thr Asn Ser Ser Arg Pro Pro Tyr
231 385             390             395             400
233 Asp Thr Pro Glu Arg Arg Pro Ser Ile Arg Met Arg Gln Gly Gly Gly
234             405             410             415
236 Gly Gly Gly Gly Gly Val Gly Val Gly Gly Met Gln Ser Gly Gly Gly
237             420             425             430
239 Gly Gly Gly Val Gly Asn Ala Lys
240         435             440
243 <210> SEQ ID NO: 4
244 <211> LENGTH: 440
245 <212> TYPE: PRT
246 <213> ORGANISM: Drosophila melanogaster
248 <400> SEQUENCE: 4
249 Met Glu Leu Arg Val Gly Asn Lys Tyr Arg Leu Gly Arg Lys Ile Gly
250  1               5               10              15
252 Ser Gly Ser Phe Gly Asp Ile Tyr Leu Gly Thr Thr Ile Asn Thr Gly
253             20              25              30
255 Glu Glu Val Ala Ile Lys Leu Glu Cys Ile Arg Thr Lys His Pro Gln
256         35              40              45
258 Leu His Ile Glu Ser Lys Phe Tyr Lys Thr Met Gln Gly Gly Ile Gly
259     50              55              60
261 Ile Pro Arg Ile Ile Trp Cys Gly Ser Glu Gly Asp Tyr Asn Val Ile
262 65              70              75              80
264 Val Met Glu Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Asn Phe Cys
265             85              90              95
267 Ser Arg Arg Phe Ser Leu Lys Thr Val Leu Leu Leu Ala Asp Gln Met
268         100             105             110
270 Ile Ser Arg Ile Asp Tyr Ile His Ser Arg Asp Phe Ile His Arg Asp
271         115             120             125
273 Ile Lys Pro Asp Asn Phe Leu Met Gly Leu Gly Lys Lys Gly Asn Leu
274     130             135             140
276 Val Tyr Ile Ile Asp Phe Gly Leu Ala Lys Lys Phe Arg Asp Ala Arg
277 145             150             155             160
```

```
279 Ser Leu Lys His Ile Pro Tyr Arg Glu Asn Lys Asn Leu Thr Gly Thr
280             165             170                 175
282 Ala Arg Tyr Ala Ser Ile Asn Thr His Leu Gly Ile Glu Gln Ser Arg
283             180             185                 190
285 Arg Asp Asp Leu Glu Ser Leu Gly Tyr Val Leu Met Tyr Phe Asn Leu
286         195             200                 205
288 Gly Ala Leu Pro Trp Gln Gly Leu Lys Ala Ala Asn Lys Arg Gln Lys
289         210             215                 220
291 Tyr Glu Arg Ile Ser Glu Lys Lys Leu Ser Thr Ser Ile Val Val Leu
292 225                 230                 235                 240
294 Cys Lys Gly Phe Pro Ser Glu Phe Val Asn Tyr Leu Asn Phe Cys Arg
295             245             250                 255
297 Gln Met His Phe Asp Gln Arg Pro Asp Tyr Cys His Leu Arg Lys Leu
298             260             265                 270
300 Phe Arg Asn Leu Phe His Arg Leu Gly Phe Thr Tyr Asp Tyr Val Phe
301         275             280                 285
303 Asp Trp Asn Leu Leu Lys Phe Gly Gly Pro Arg Asn Pro Gln Ala Ile
304         290             295                 300
306 Gln Gln Ala Gln Asp Gly Ala Asp Gly Gln Ala Gly His Asp Ala Val
307 305             310                 315                 320
309 Ala Ala Ala Ala Ala Val Ala Ala Ala Ala Ala Ala Ser Ser His Gln
310             325                 330                 335
312 Gln Gln Gln His Lys Val Asn Ala Ala Leu Gly Gly Gly Gly Gly Ser
313             340             345                 350
315 Arg Ala Gln Gln Gln Leu Gln Gly Gly Gln Thr Leu Ala Met Leu Gly
316         355             360                 365
318 Gly Asn Gly Gly Gly Asn Gly Ser Gln Leu Ile Gly Gly Asn Gly Leu
319         370             375                 380
321 Asn Met Asp Asp Ser Met Ala Ala Thr Asn Ser Ser Arg Pro Pro Tyr
322 385             390                 395                 400
324 Asp Thr Pro Glu Arg Arg Pro Ser Ile Arg Met Arg Gln Gly Gly Gly
325             405             410                 415
327 Gly Gly Gly Gly Gly Val Gly Val Gly Gly Met Gln Ser Gly Gly Gly
328             420             425                 430
330 Gly Gly Gly Val Gly Asn Ala Lys
331         435                 440
334 <210> SEQ ID NO: 5
335 <211> LENGTH: 72
336 <212> TYPE: DNA
337 <213> ORGANISM: Drosophila melanogaster
339 <400> SEQUENCE: 5
340 ataggatcgg gatcgttcgg cgacatctac ctgggcacca cgatcaacac tggcgaggag 60
341 gtggccatca ag                                                    72
343 <210> SEQ ID NO: 6
344 <211> LENGTH: 24
345 <212> TYPE: PRT
346 <213> ORGANISM: Drosophila melanogaster
348 <400> SEQUENCE: 6
349 Ile Gly Ser Gly Ser Phe Gly Asp Ile Tyr Leu Gly Thr Thr Ile Asn
```

FYI.

Use of n and / or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
to ensure a corresponding explanation is present
in the <220> to <223> fields of each sequence
using n or Xaa.

VERIFICATION SUMMARY   DATE: 07/20/2001
PATENT APPLICATION: US/09/559,867   TIME: 14:19:37

Input Set : **A:\600221nc.app**
Output Set: **N:\CRF3\07202001\I559867.raw**

L:14 M:270 C: Current Application Number differs, Replaced Current Application Number
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40